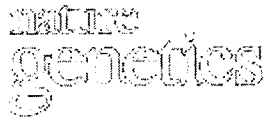


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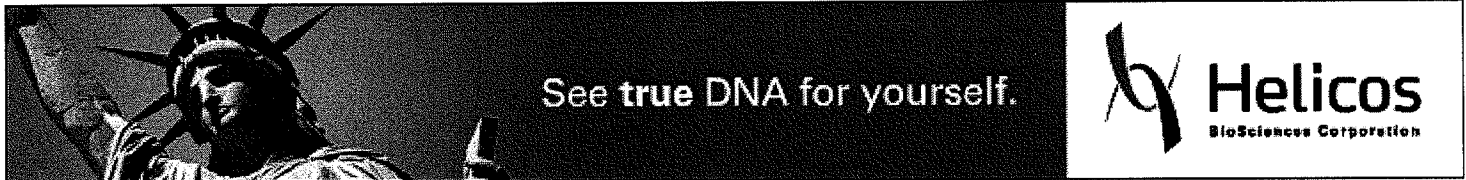
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Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression

Kousaku Okubo¹, Naohiro Hori¹, Ryo Matoba¹, Toshiyuki Niiyama¹,
Atsushi Fukushima¹, Yuko Kojima¹ & Kenichi Matsubara¹

¹Institute for Molecular and Cellular Biology, Osaka University, 1-3 Yamada-oka, Suita,
Osaka, 565 Japan

Large scale sequencing of cDNAs provides a complementary approach to structural analysis of the human genome by generating expressed sequence tags (ESTs). We have initiated the large-scale sequencing of a 3'-directed cDNA library from the human liver cell line HepG2, that is a non-biased representation of the mRNA population. 982 random cDNA clones were sequenced yielding more than 270 kilobases. A significant portion of the identified genes encoded secreted proteins and components for protein-synthesis. The abundance of cDNA species varied from 2.2% to less than 0.004%. Fifty two percent of the mRNA were abundant species consisting of 173 genes and the rest were non-abundant, consisting of about 6,600 genes.

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